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March 20, 2004, 17:42:00 ; Search time 6486 Seconds (without alignments) 10932.656 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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is the Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahadi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Rurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sudyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
Kawai, J., Carninci, P., Adachi, J., Alzawa, K., Arakawa, T., Fukuda, S., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Shiraki, T., Saito, R., Shiraki, T.,
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Oryza sativa (japonica cultivar-group) cDNA clone:J023043123, full insert sequence.

AK070211. GI:32980235

FILCONA, CAP trapper.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Enharyota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Gaps

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328

407 388 467 448

527 487 587 547 647 607 707 667 767 727 827 787 887 847

MEDLINE FUBMED REFERENCE AUTHORS

JOURNAL

TITLE

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TTATACTGCACAGTGTGCTATCAATCGTTGCCAGCACTGGACAAAGGTCTGCGAGTCTCA 1187
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Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Azakawa,T., Carninoi,P., Fukuda,S., Hanagaki,T., Hara,A., Hashitume,W., Hayashida,K., Havashida,K., Haranta,T., Azakawa,T., Carninoi,P., Kuda,M., Kanagawa,T., Kanagawa,K., Harashida,K., Inotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kanagawa,T., Kondo,S., Konno,H., Konda,M., Kishikawa-Hirozane,T., Kanagawa,T., Miyazaki,A., Murata,M., Nakai,K., Nomura,K., Numasaki,R., Ohno,H., Sato,K., Saltoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Tagawa,A., Takahashi,F., Yasunishi,A., and Hayashizaki,Y.
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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
URA: skice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Shikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
205-8602, Japan (E-mail:sKiuchi@mias.affrc.go.jp,
78-181-29-838-7007, Fax: 18-29-838-7007, This clone is one of the 28K full-length cDNA clones from japonica
                                              over 28,000 cDNA clones
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="J023043123"
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Pred. No. 9.5e-161;
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of
japonica rice
Science 301 (5631), 376-379 (2003)
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TLQFNNSVPTPYVPMRRELKAAQSDKQLGLESFILELSLVBYQMLKYRPSLLSAAAV
YTAQCALTRCQQATTTCELLASRYTGGQLLECSRMMVDFHQKAGAGKLTGVHRKYSTFK
FGCAAKTEPALFLLESGAGGYNLQKOPC"
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Oryza sativa cycB2;os;l mRNA for cyclin, complete cds.
AB024987
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Uchimiya,H.
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db_xref="G1:6331704"
'translation="MDRASENRRLAAVGKPVPGIGEMGNRRPLRDINNLVGAPSHPSA
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NPIPDGTVDDDVESCESNDYIAVDECNDTDEDESMMDIDSADSGNPLAATEYVEELYK
FYRENEEMSCVQPDYMSSQGDINEKMRAILIDWLIEVHHKFELMDETLFLTVNIVDRF
                                             1248 GAAGGCTGGAACCAGTAAGCTCACTGGCGTGCACAGGAAGTACAGTACCTACAAGTTCGG 1307
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   TAGCAGATACACTAGCGACCAACTCCTGGAGTGCTCGAGGATGATGGTAGATTTTCACCA 1247
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-MAR-1999) Masaaki Umeda, University of Tokyo, Institute of Molecular and Cellular Biosciences; Yayoi 1-1-1, Bunkyo-ku, Tokyo 113-0032, Japan (E-mail:mumeda@imcbns.iam.u-tokyo.ac.jp, Tel:81-3-5841-8466,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular characterization of mitotic cyclins in rice plants Mol, Gen. Genet. 262 (2), 230-238 (1999)
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|mol_type="mRNA"
|strain="Yamahoushi"
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Location/Qualifiers
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                          TAGTAGATATACCGGAGAGCAGCTTCTTGAGTGTTCTAGGATGATGGTAGATTTCCACCA 1194
                                                                                                          GAAGGCGGGAGCAGCCAAGCTCACCGGCGTGCACCGGAAATACAGTACGTTCAAGTTTGG 1254
                                                                                                                                                              TTGCGTGGCCAAGATTTTGCCTGCGCAGTTCCTGCTGGAGTCGGGAG--GGACACCGCCT 1365
                                                                                                                                                                                                        GTGTGCAGCCAAAACGGAGCCTGCTCTTCTTGCTTGAGTCAGGAGCAGGAGGTTACAA 1314
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University, East Lansing, MI 48824-1312,
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                                                                                GAAGGCTGGAACCAGTAAGCTCACTGGCGTGCACAGGAAGTACAGTACCTACAAGTTCGG
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Pred. No. 7.2e-110;
); Mismatches 159; Indels 2;
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/organism="Oryza sativa"

/mol_type="marNA"

/db_xref="taxon:4530"

/tissue_type="internode sections"

/clone lib="lambda ZAPII cDNA"

/dev_stage="mature plant"
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O.sativa mRNA for cyclin 1.
X82035.1 GI:558620
Cyclin; cycOs1 gene.
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Submitted (04-0CT-1994) H.
Laboratory, Michigan State
USA
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llarity 79.0%;
Conservative (
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AUTHORS
TITLE
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OSCYCOS1
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AK070518
Oryza sativa (japonica cultivar-group) cDNA clone:J023055K12, full insert sequence.
AK070518
AK070518.1 GI:32980542
Full CDNA, CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidese; Oryzea.
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                                                                                   TCTTGGAAAAGGAGTTCCAAGGAAGAAGCTACAACTGGTTGGAGTCACAGCTATGC
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Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fuluda, S., Hangaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayashizu, M., Hiramoto, K., Hiraoka, T., Hotta, I., Idda, Y., Ikada, R., Imamura, K., Imbibiki, J., Ishik, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kangawa, S., Katoh, H., Kawagashira, M., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kohan, M., Kawai, J., Kawamata, M., Kodama, T., Kojima, Y., Kojima, Y., Kojima, M., Kojama, T., Kojima, Y., Kojima, M., Kojama, T., Kojima, Y., Kojima, M., Matsubara, K., Murakami, K., Sakai, K., Sakai, K., Sakai, M., Sakai, D., Sakai, M., Sakai, D., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Shibata, K., Tagami, Tagami, Takeda, Y., Tagawa, A., Takahashi, F., Tagami, M., Tagami, Takeda, Y., Yanamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,O., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Milra,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RiksN.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RiksN.,
Hashidunci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidunci,W., Hayatsu,N., Imotani,K., Ishi,YY., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 301 (5631), 376-379 (2003)
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MEDLINE
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AUTHORS
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Pals Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fals Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Kodamara,M., Kobayashi,M., Kodayashi,M., Kodamara,Y., Kucosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Kyu,R., Sugano,S., Sugiyama,A., Buzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Science Laboratory in Riken Genomic Science Caboratory in Riken Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carnicci,P., Fukuda,S., Harawa,K., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hara,A., Hashizume,W., Hayashida,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,K., Ishii,Y., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Kishikawa-Hirozane,T., Miyazaki,R., Ohno,M., Osato,N., Sasaki,D., Satoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,C., Sato,K., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Shibata,K., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                            URL : http://cdnaol.dna.affrc.go.jp/cDNA/
MAGS Rice Full-Length cDNA project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kampondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mas.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
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PLN 13-FEB-1998

linear

mRNA

1793 bp

O.sativa mRNA for cyclin 2. X82036 Y09038

OSCYCOS2

LOCUS

FEATURES

RESULT 6 OSCYCOS2

ACCESSION

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1021 GATGCAGATAAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGGTAGAA 1080
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                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
/organism="Cryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                                               8; Length 1777;
                                                                                                                                                                                                                                                                                               tch 124.6%; Score 402.2; DB 8; Length 1
al Similarity 68.6%; Pred. No. 1.38-86; S54; Conservative 0; Mismatches 253; Indels
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/ product="acyolin"
/ protein id="ca24556.1"
/ protein id="ca2492"
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X82036.1 GI:1694891
Cyclin; cycOs2 gene.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
E 1 (bases 1 to 1418)
Sauter, M., Mekhedov. S.L. and Kende, H.
Gibberellin promotes histone H1 kinase activity and the expression of edc2 and cyclin genes during the induction of rapid growth in deepwater rice internodes
L Plant J 7 (4), 623-632 (1995)
D 7742859
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Submitted (04-OCT-1994) H. Kende, MSU-DOE Plant Research
Laboratory, Michigan State University, Bast Lansing, MI 48824-1312,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sauter, M. state and characterization of a cDNA encoding a mitotic cyclin of the CycB2 type from rice (accession no. X82036) Unpublished
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22609 Hamburg,
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Ref [5]: Plant Gene Register PGR97-001 (1997).
Location/Qualifiers
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Direct Submission
Submitted (26-NOV-1996) M. Sauter, Univ. Hamburg,
Allgemeine Botanik, AMPII, Ohnhorststrasse 18, D-
FRG
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/organism="Oryza sativa"
/mol type="RAM"
/cullivar="Pindaew5"
/db xref="teaxon:4530"
/tisue type="internode sections"
/clone_lib="lambda ZAPII cDNA"
/dev stage="mature plant"
1. 1793
/gene="cyc0e2"
/gene="cyc0e2"
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24.5%; Score 400.6; DB 8;
Best Local Similarity 68.5%; Pred. No. 3.1e-86;
Matches 553; Conservative 0; Mismatches 254;
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5 (bases 1 to 1793)
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sativa L
Unpublished
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1020

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MSCYCMS2
M.sativa CYCMS2 mRNA for cyclin.
X68741 S13352
X68741.1 GI:19598
Cyclin, cyclin homolog.
Medicago sativa
Medicago sativa
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermarcphyta; Magnoliophyta; eudicotyledons; core eudicots;
Cosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Gartner, A., Dudits, D. and Heberle-Bors, E.
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MVCYCMS2 1758 bp M.varia mRNA for mitotic cyclin 2.
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/protein_id="CAA57560.1"
/db_xref="GI:914863"
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RASIVOWSDLIHTADRAYMKEDILEMPMLIDRFLAKQWVWFKKLQLVGEVAMLLAKYY
KLELVAFELVOLSILHTADRAYMKEDILEMPMLANTLOWNSLPTAYVFMRFLKAQADK
KLELVAFELVDLSYLEWERPPSIVAAAAYYTAQCTYSGFKHWNKTCEMHYNYSED
QLLECSMLMVGFHQKAGAGKLTGVHRKYGSAKFSFTAKCEPACFLLENKNQP"
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Alfalfa cyclins: differential expression during the cell cycle and in plant organs Plant Cell 4 (12), 1531-1538 (1992) 93109677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 GAGTATATTGAAGATCTCCATGCTTACTACAGAAGATTGAGTATCTTGGCTGTGTTTCA 264
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                                                                                                                                                                                                                                                                                                                        gene="CYCMS2"
note="Cyclin homolog of B type. Cyclin B is associated
with CDC2 kinase and regulates entry and exit into and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 GAAGATGATTGCTCATGGATATTGACAGTGCAGACTCGGGGAACCCGCTTGCTGCAACA
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                                                                                                                                            Univ of
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                                                                                                                   Direct Submission
Submitted (14-OCT-1992) H. Hirt, Inst of Microbiology, Usenna, Biocenter, Dr Bohrgasse 9, 1030 Vienna, AUSTRIA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8; Length 1343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 383.4; DB 8; Length 1
Pred. No. 4.5e-82;
0; Mismatches 276; Indels
                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                  /organism="Medicago sativa"
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                                                                                                                                                                                                                                                                                       gene="CYCMS2"
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ilarity 66.5%;
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                                                                                                       Hirt, H.
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VHDREDLMOETLELTVNLIDDRELAKONVVRKKLQLVGLVAMLLACKYEEVSVPVVSDL
IHIDAATREKDILERSKLMLNTLOYNGSPPAYVEWERFELKAAQADKKLELVAFFLV
DLSLVEYEMIKFPPSLVAAAAVYTAQCTVSGFKHWNKTCEWHTNYSEDQLLECSMLMV
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Submitted (04-OCT-1994) M. Pirck, Inst for Microbiology & Genetics,
University of Vienna, Dr. Bohrg. 9, 1030 Vienna, AUSTRIA
Related sequences: X68740, X68741, S53351 and S53352.
Location/Qualifiers
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Medicago sativa subsp. x varia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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cyckaß, a novel B-type alfalfa cyclin gene, is induced in the GO-to-G1 transition of the cell cycle
Plant Cell 7 (6), 759-771 (1995)
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/mol_typo="mRNA"
/sub_species="A2"
/dbxref="taxon:36902"
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 GFHQKAGAGKLTGVHRKYGSAKFSFTAKCEPACFLLENKNQP"
209. .235
//gene="deycM82"
/note="destruction box"
                                                                                                     Indels
                                                                           Score 383.4; DB 8;
Pred. No. 4.8e-82;
0; Mismatches 276;
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PLN 18-SEP-1995

linear

mRNA

MSCYC12 1706 bp M.sativa mRNA for B-like cyclin. X78504 X78504.1 GI:780266

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Medicago sativa
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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llarity 65.9%; Pred. No. 9.1e-80;
Conservative 0; Mismatches 280; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="young nodules"
/clone lib="lambda ZAP II"
1. .1706
                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Medicago sativa"
                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (29-MAR-1994) A. Savoure
Vigitales, Avenue de la Terrasse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /haplotype="tetraploid"
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/sub_species="varia"
/db_xref="taxon:3879"
/clone="AS9D"
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1. .1706
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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GTCACAGCTATGCTGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGAC 885
                                                                                                                                                                    CTAGTGGCAATGCTTTTGGCATGCAAGTATGAGGAAGTTTCAGTGCCTGTGGTTTGGAGAT 949
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Plant Cell 7 (6), 759-771 (1995)
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1. 1700

/. 1700
/organism="Medicago sativa subsp. x varia"
/sub_species="mRNA"
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FDLWHETLEFLYVNLIDRFLEKQSVYRKKLQLVGIVAMLLAGKYEBYSYPVGDLILIS
DRAYTRKEVLEMEKVMVNALKFNISVPTAYVFMRRELKAAQADRKLELLAFFLIELSL
VEYAMLKREPSQLAAAVYTAQCTRYGVKOWKTCEWHTNYSEDQLLECSSLAVDFHK
KAGTGKLIGAHRKYCTSKFSYTAKCEPASFLLENEL
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PYPCVVNKRALSERNDVCEKKQADPVHRPITRRFAAKIASTKTSNAEGTTKRSNLAKS
SSNGFGDFIFVDDEHKPVEDQPVPMALEQTBPMHSESDQMEEVEMEDIMEEPVMDIDT
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22.8%; Score 372.4; DB 8; Length:
Best Local Similarity 65.8%; Pred. No. 2.2e-79;
Matches 541; Conservative 0; Mismatches 281; Indels
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/db_xref="G1914861"
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//protein id="CAB46645.1"
//protein id="CAB46645.1"
//db xref="G1:542022"
//db xref="G03:03G21"
//db xref="G0A:03G21"
//db xref="G0
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LULISDKAYTRKEVLEMESMALINTLÖPRNGVPFAYVERRRYLKRAQCDRKLELLSFML
VELCLVETENLKPPSFIAARATYTAQTTLYCVQWRSTCEVHTTYSEDQLLECSRSI
VGYHQKAATGKLTGVHRKYSISKFGYAAKCEPAHFLVQQTQE"
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Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
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Submitted (01-UUL-1999) Chevalier C., Unite de Physiologie
Vegetale, Institut National de la Recherche Agronomique, B.P. 81,
33883 Villenave d'Ornon cedex, FRANCE
Location/Qualifiers
1. .1999
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CACACCAACTACTCTGAAGATCACTCTTAGAATGCTCTAGTTTAATGGTTGACTTTCAC
                                                                                 CAGAAGGCTGGAACCAGTAAGCTCACTGGCGTGCACAGGAAGTACAGTACCTACAAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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/mol_type="MENA"
/coltivar="West Virginia 106"
/db_xref="taxon:4081"
/tissue_type="fruit"
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Arabidopsis thaliana (thale cress)
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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Location/Qualifiers
1. .1255
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Hlavskralsekpaaaaanakdoageyghpytrkfaatlatoptyalldbigser
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Submitted (25-MAY-1994) Venkatesan Sundaresan, Cold Spring Harbor
Laboratory, P.O. Box 100, 1 Bungtown Road, Cold Spring Harbor, NY
11724, USA
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GTGCACAGGAAGTACAGTACCTACAAGTTCGGTTGCGTGGCCAAGATTTTGCCTGCGCAG
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/clone_lib="Lambda_ZAPII, library of B. Veit
/dev_grage="immature"
17. 1291
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Pred. No. 1.2e-75;
0; Mismatches 285; Indels
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/product="cyclin IIIZm"
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/db_xref="GI:516548"
                                                                                                                                                                                                1603 bp
cyclin IIIZm mRNA,
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1. 1603
7 organism="Zea mays"
/mol type="mRNA"
/strain="B73"
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691 615 751 675 811 871

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976 GITCCAACACCITAIGICITCAIGAAGAGGITICIGAAAGCIGCAGAIGCAGAIAACAG 1035
1112 CIACCAACCCAATGITITCAIGAAACGAITICICAAAGCIGCCCAAICIGACAAGAAG 1171
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                                                                                                                                                                               GACTCGGGGAACCCGCTTGCTGCAACAGAATATGTTAAAAGAGCTTTACACCTTTTACAGA
Query Match
21.8%; Score 357; DB 6; I
Best Local Similarity 63.7%; Pred. No. 1.2e-75;
Matches 543; Conservative 0; Mismatches 310;
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Location/Qualifiers
1.1287
/organisme="Arabidopsis thaliana"
/mol type="unassigned DNA"
/db_xref="taxon:3702"
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Best Local Similarity 63.9%;
Matches 539; Conservative
Arabidopsis thaliana
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Oy 1281 CAGGAAGTACCTACAAGTTCGGTTGCGTGGCCAAGATTTTGCTGCGGAGTTCT 1340

Db 1206 TAGGAAGTACAAGCAAATTTGGTTACATAGCAAAATGTGAAGCTGCACTTTTT 1265

Qy 1341 GCTG 1344

Db 1266 AGTG 1269

Search completed: March 20, 2004, 21:50:17

Job time: 6491 secs
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March 20, 2004, 15:08:29 ; Search time 674 Seconds (without alignments) 10311.650 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-496-444-1 1636 1 tcacggggctcctccgtccgaaaaaaaaaaaaaa	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	3373863 seqs, 2124099041 residues	Total number of hits satisfying chosen parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	œ			Arabi	Add15948 cDNA (Seq	_	•		•	Human	Human		Aav83711 Nucleic a	Abk12023 Human cyc	Abi99379 Mouse isc	Aag37741 Complete		Abl62877 Breast ca			Abl62671 Colon ade	m	Abt10909 Human bre
	ΩI	C83	AAS96272	AAS96310	AAS96276	ADD15948	ABX81803	ABZ12984	AAC83106	AAC42253	AAC77911	AAH14263	ACH03960	AAV83711	ABK12023	AB199379	AAQ37741	AAV30100	ABL62877	ABL67953	ABL65385	ABL62671	ABL65823	ABT10909
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ABN95810	AAI59816	AA158030	ACC51016	ACC44992		AAT41775	ABT18843	, ABT18249	, ABT20663	ABT20065	, ABT17655	ABT19469	, ABZ19165	ADD17214	2 AAQ13385	2 AAV16888	2 AAX26023	3 AAZ87508	4 AAS03727	5 ABL69120	4 ABL20111
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ALIGNMENTS

RESULT 1

Sun Y; Helentjaris TG, Habben JE, WPI; 2000-687333/67. P-PSDB; AAB35801.

Nucleic acids useful for producing transgenic plants, preferably maize, with increased cell cycle gene activity, preferably activity of cyclin and/or cyclin-dependent kinase.

Claim 1; Page 104-106; 122pp; English.

Polymucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 - AAB35806 which are involved in regulating the cell cycle. The protein and DNA sequences have been isolated from Zea may8 (corn), and the invention also includes oligonucleotides AAC83114 - AAC83139 which are related to the cell cycle polymucleotides. The cell cycle polymucleotide sequences are useful for producing transgenic plants such as maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet with increased levels of cell cycle gene activity, such as activity of cyclin and cyclin-dependent kinases. The DNA sequences are

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New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.
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GTGCTGATATCTGACCGTGCCTACACAAAAGGGCAAATTTTAGAAATGGAAAAGTTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell cycle protein; CCP; ss; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic nutrient deprivation; pathogen attack; crop yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis cDNA encoding partial cell cycle protein CCP1.
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P-PSDB; AAU72482.
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   also useful as probes for detecting deficiencies in the level of mRNA in screening for desired transgenic plants, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detecting any number of allelic variants, orthologs or paralogs of the gene, and site-directed mutagenesis in eukaryotic cells. The DNA sequences are also useful for recombinant expression of the encoded polypeptides and as immunogens for preparing and screening antibodies. A transgenic plant comprising an expression cassette including a cell cycle regulatory gene is useful for assaying enzyme agonists and antagonists, and as immunogens or antigens to obtain antibodies. The antibodies are useful in assaying expression contains of levels of cell cycle regulatory proteins, for identifying and isolating nucleic acids from expression libraries, for identifying homologues of polypeptides from other species, and for purification of the proteins
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1275; Conservative 0; Mismatches 0; Indels 0
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The invention relates to a novel cell cycle protein (CCP) and the polymucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and anti-CCP antibody is useful for modulating the cell cycle protein the polypeptide and anti-CCP antibody is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana. Tice, wheat, maize, comato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat dioorders characterised by insufficient or excessive production of CCP protein forms which have decreased or portained activity. Compounds that bind to or modulate the activity of CCP protein forms which have decreased or polymucleotide is useful for modifying cell fate, plant development, plant morphology, blochemistry and/or physiology, the length of the G1, S, Gz and/or phase of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, shoot and root initiation and or development, nodule function, dwarfism in plants, contained in and/or development, nodule function, dwarfism in plants, contains a contained by a protein involved in the cell cycle due to environmental conditions, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or bacies stress such as cord activity of a protein involved in the cell cycle development and parts, including abiotic stress such as cold, nutrient deprivation, heat, drought, salt stress, or bacies stress such as manuscent cold pants, and parts, sold stress or better such as cold, nutrient deprivation, heat, drought, salt stress, or bacies stress such as immunogen to generate antibodies. CCP protein is useful to screen for naturally contained to modulate is useful to screen for protein of modulate cCP modulate e.g. enhance crop yields, and to modulate of m

Sequence 1255 BP; 427 A; 214 C; 274 G; 340 T; 0 U; 0 Other;

.; 0 Score 357; DB 6; Length 12 Pred. No. 4.9e-84; 0; Mismatches 310; Indels 21.8%; Conservative Similarity Matches 543; Query Match

496 GCGACAGAGAACAATATGAACGAAGATGAATTGCTCATGGATATTGACAGTGCA 555 172 GAGATTGAAATGGAAGATGCAGACAAAGAAGAAGAGGCCTGTGATGATGATGTTGATGCCTGT qq à

292 AATTTTGAGAAACTTAGTTGCGTGCCTCCTAACTATAGGACAATGACAAGACTTTAAT 351 GAAAATGAGGCTAAGAGTTGTGTAAGGCCAGATTACATGTCCAGCCAACAAGACATAAAC TCAAAGATGAGGCAATTCTGATTGACTGGCTGATTGAGGTTCACTACAAGTTTGAACTG 919 919

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AAS96310 standard; cDNA; 1715 BP. AAS96310; RESULT 3
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(first entry) 26-FEB-2002

Arabidopsis cDNA encoding cell cycle protein CCP1.

Cell cycle protein; CCP; ss; cell cycle regulation; herbicide; plant growth regulator; plant development; abiotic stress; biotic stress; nutrient deprivation; pathogen attack; crop yield.

Arabidopsis thaliana.

WO200185946-A2.

15-NOV-2001.

14-MAY-2001; 2001WO-IB001307. 12-MAY-2000; 2000US-0204045P.

(CROP-) CROPDESIGN NV.

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Magyar Acosta JAT, Veylder L, De. Boudolf V, Inze D,

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WPI; 2002-062249/08. P-PSDB; AAU72520.

New cell cycle protein and nucleic acid molecule encoding it useful fregulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators.

Claim 38; Fig 1; 316pp; English

The invention relates to a novel cell cycle protein (CCP) and the polynucleotides encoding them. CCP is useful for identifying a compound which modulates the activity of the polypeptide and which binds to the polypeptide and an anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat, maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola. CCP

cc nucleic acid and polypeptide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or production of CCP protein forms which have decreased or polypeptide are useful for polyment to or modulate the activity of CCP polypeptide are useful for modifying cell fate, plant development, polymential as herbicides or plant growth regulators. The collymucleotide is useful for modifying cell fate, plant development, by an analysis of the cell cycle of a plant, initiation, promotion, stimulation or enhancement of cell division, DNA replication, seed set, seed development, tuber, fruit, leaf formation, shoot and root initiation and/or development, tuber, fruit, leaf formation, shoot and root initiation and/or development, nodule function, dwarfism in plants, sensescence, tolerance or resistance to stress. CCP, the polymucleotide conditions, including abiotic stress such as cold, mutrient protein levels or activity of a protein involved in the cell cycle due to protein levels or activity of a protein inspects stress such as cold, mutrient conditions, including abiotic stress such as cold, mutrient conditions, including abiotic stress such as cold, mutrient conditions, including abiotic stress such as cold, mutrient conditions in storage cells, storage tissues and/or storage organs of plants or its parts. CCP is useful as an immunogen to storage organs of plants or its parts. CCP is useful as an immunogen condensation, to detect CCP mRNA, or a genetic lesion in a CCP gene and to protein, to detect CCP mRNA, or a genetic lesion in a CCP gene and to invention 8888888888888888888888888888888888

Sequence 1715 BP; 585 A; 290 C; 370 G; 470 T; 0 U; 0 Other;

CTIGAGALTITAICATICTITAIGATCGAGCTITGCCTIGTGGAGTATGAGAIGCTAGAG 1231 GITCCAACACCITATGTCTTCATGAAGAGGTTTCTGAAAGCTGCAGATGCAGATAAACAG 1035 CTACCAACTCCATATGTTTTCATGAACGATTTCTCAAAGCTGCCCAATCTGACAAGAAG 1171 ö 992 gaagaagtriccagriccagragargarcricarcrigarcricagaaagcriacric 1051 975 GAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCTGACCGTGCCTACACA 915 GCGACAGAGAACAAGGACATTATGAACGAAGATGAATTGCTCATGGATATTGACAGTGCA 555 691 615 daraadaaradricerrindderdeegerrdadrarareedradaaradeeraeerrieraedag 751 675 811 735 871 931 991 872 ArdeAgdAAACTCTTAATCTCACAATCAATGTCATCGACAGATTCCTTGCGGTTCATCAA 676 TCAAAGATGAGGAATTCTGATTGACTGGCTGATTGAGGTTCACTACAAGTTTGAACTG 812 GAGAGAATGAGAAGGAATCCTCATTGACTGGTTAATTGAGGTGCACTACAAGTTTGAACTG 932 Arcgreaddaaaaadcrrcaccrrcidergraracrecrrigeridergcardraaarar AAAGGGCAAATTTTAGAAATGGAAAAGTTGATTCTGAACACGCTGCAGTTCAACATGTCT agaagagaagaagararagagaagaagcaaragaccaacaccaaricaarricaarricaarricaarricaarricaarricaarricaarricaarricaarricaar GAAAATGAGGCTAAGAGTTGTGTAAGGCCAGATTACATGTCCAGCCAACAAGACATAAAC AATTTTGAGAAACTTAGTTGCGTGCCTCCTAACTATATGGACAATCAACAAGATCTTAAT 796 GTTCCAAGGAAGAAGCTACAACTGGTTGGAGTCACAGCTATGCTGCTCGCTTGTAAATAT GACTCGGGGAACCCGCTTGCTGCAACAGAATATGTTAAAAGAGCTTTTACACA GAGATTGAAATGGAAGATGCAGACAAAAAAAAAAAAGAAGACCTGTGAATCGATATTGATGCCTGT Gaps ; 0 Score 357; DB 6; Length 1715; Pred. No. 5.7e-84; O; Mismatches 310; Indels 21.8%; al Similarity 63.7%; 543; Conservative Query Match Best Local Si Matches 543, 856 (916 1052 946 1112 1036 1172 752 736 632 556 g ద à d 8 g δ g ò d ò , q d 셤 à 충 ð ò ò

The invention relates to a novel cell cycle protein (CCP) and the polymucleotides encoding them. CCP is useful for identifying a compound polymucleotides the activity of the polymetide and which binds to the polymetide and which binds to the oplypeptide and anti-CCP antibody is useful for detecting the presence of CCP in a sample. A CCP modulator is useful for modulating the cell of cycle or growth of a plant such as Arabidopsis thalians, rice, wheat, compared and polymetide molecules are useful as modulating agents in nucleic acid and polymetide molecules are useful as modulating agents in regulating cell cycle progression in plants. CCP is useful to treat cisculating cell cycle progression in plants. CCP is useful to treat disorders characterised by insufficient or excessive production of CCP protein forms which have decreased or protein or production of CCP protein forms which have decreased or compensate are useful as nectivity of CCP polymetides are useful as herbicides or plant growth regulators. The polymucleotide is useful for modifying cell fate, plant development, plant morphology, biochemistry and/or physiclogy, the length of the G1, 1411 GIGCACAGGAAGIACAGIACCIACAAGIICGGIIGCGIGGCCAAGAIITIIGCCIGCGCAG 1335 TATCGGCCTTCGCCATCTGGCTGCTGCTGCTATATACTGCACAGTGTGCTATCAATCGT 1155 1232 rarictrickarkraageregeserkageaarerakkakrigereagigrakakrinaaga 1291 Cell cycle protein; CCP; ss; cell cycle regulation; herbicide; plant growth regulator; plant development; abictic stress; bictic stress; nutrient deprivation; pathogen attack; crop yield. New cell cycle protein and nucleic acid molecule encoding it useful for regulating cell cycle progression in plants and for identifying modulators which are useful as herbicides or plant growth regulators. GAGTGCTCGAGGATGGTAGATTTTCACCAGAAGGCTGGAACCAGTAAGCTCACTGGC trrgaagaarddaacaaaacchdrdadarrrcacacadcracaacaaaaacadcracrd TGCCAGCACTGGACAAAGGTCTGCGAGTCTCATAGCAGATACACTAGCGACCAACTCCTG ź Magyar Arabidopsis cDNA encoding cell cycle protein CCP5. Acosta JAI, De Veylder L, AAS96276 standard; cDNA; 1287 BP Claim 38; Fig 6; 316pp; English. 14-MAY-2001; 2001WO-IB001307. 12-MAY-2000; 2000US-0204045P. TTCCTGCTGGAGT 1348 TITCIGATITAAT 1484 (first entry) (CROP-) CROPDESIGN NV Arabidopsis thaliana. Inze D, Boudolf V, 2002-062249/08. P-PSDB; AAU72486 WO200185946-A2. 26-FEB-2002 15-NOV-2001. 1096 1292 1216 1352 1276 1412 1336 1472 1156 AAS9627 g ठ 유 셤 ò 셤 à 유 à

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stimulation or enhancement of cell division, DNA replication, seed set, seed development, tuber, fruit, leaf formation, seed set, seed development, tuber, fruit, leaf formation, seed set, initiation and/or development, nodule function, dwarfism in plants, senescence, tolerance or resistance to stress. CCP, the polymucleotide and the anti-CCP antibody are useful in agriculture to modulate the protein levels or activity of a protein involved in the cell cycle due to environmental conditions, including abicic stress such as cold, mutrient deprivation, heat, drought, salt stress, or biotic stress such as pathogen attack, to modulate e.g. enhance crop yields, and attenuate plant architecture, plant quality traits, plant reproduction and seed development, endoreduplication in storage crop yields, and immunogen to generate antibodies. CCP protein is useful to screen for naturally contraining CCP protein, to detect CCP many, or a genetic lesion in a CCP gene and to modulate CCP activity. The present sequence encodes a CCP protein of the
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Pred. No. 9.2e-84;
0; Mismatches 305; Indels
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Best Local Similarity 63.9%;
Matches 539; Conservative
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This invention relates to the identification and isolation of movel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wer leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel penorypes can affect growth regulation i.e. useful for creating dwarf varieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or calculated sensescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the phenotype of plants seeds, plant tissues and plant cells containing the conting cDNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                1206 naddaadracadcacacaadcaaaririddriacaradcaaaarorgaagcridcacarrircr
                                                                1146 Trcacechaecrecresererecarchecaecececeacaecaeaaacriaacaecaarata
1221 CTCGAGGATGATGGTAGATTTTCACCAGAAGGCTGGAACCAGTAAGCTCACTGGCGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; visual phenotype; plant; architecture; leaf surface; chlorotic; bleaching; etching; wet leaf; stunting; elongation; texture; agronomic trait; growth regulation; dwarf variety; insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA (SeqID 16) that confers an altered visual phenotype in plants
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Pred. No. 2.2e-69;
0; Mismatches 198;
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                                                                                                                                       CAGGAAGTACAGTACCTACAAGTTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD15948 standard; cDNA; 627
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                                    2 AAAAATGGAGGGTTGCAGTCGCCAGACTATATGGCACAACAGTTTGACGTCAA 61
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615 AGAAAATGAGGCTAAGAGTTGTGTAAGGCCAGATTACATGTCCAGCCAACAAGACATAAA
                                                                                                                                                                                                                                   GGTTCCAAGGAAGAAGCTACAACTGGTTGGAGTCACAGCTATGCTGCTCGCTTGTAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AGTTCCAACTCCATATGTTTTTATGAGAAGATTTCTCAAAGCTGCTCAATCAGATAAAAA
                                                                            675 CTCAAAGATGAGAGCAATTCTGATTGACTGGCTGATTGAGGTTCACTACAAGTTTGAACT
                                                                                                              Corn ear-derived polynucleotide (cpd) #263.
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The present invention relates to the isolation of corn ear-derived polymuclectides (cdps) from the corn (Zea mays) cDNA libraries SATMONO22 and SATMONO23. Some of the cpds uniquely identify structural, functional, and standardry genes of corn ear. The polymuclectides sequences are useful for detecting cpds in a sample, for producing a corn ear specific profile of gene transcription, for detecting altered gene expression in inbred or hybrid plants, and for screening several molecules for specific binding to the polymuclectide. The cdps are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridisation techniques of the sylvasion of desirable traits through plant breeding programs. Perferably, the cdps are used to identify, evaluate, alter, or follow the inheritance of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality, and yield of corn. The cdps are also useful in field properides by recombinant techniques. They are also useful in disgnostic assays to recombinant techniques. They are also useful in disgnostic assays to recombinant techniques. They are also useful in disgnostic assays to detect or confirm conditions or diseases associated with abnormal levels of cdp expression. Abx81641-Abx89140 represent corn ear-derived polymuclectides (cpds) of the invention. Note: The sequence data for this pectual disease associated with abnormal levels of petent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at
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                                                                                                                                                                      Novel purified corn-ear derived polynucleotide useful as hybridization probe for detecting polynucleotide in sample, and for identifying, evaluating, and altering desired characteristics associated with growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GCTATTTCTTACGGTAAACGTAATAGATAGATTCTTGGAAAAAGGAAGTGGTTCCAAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 274 BP; 82 A; 47 C; 67 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                 Example; SEQ ID NO 263; 390pp; English.
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                                                                            Sherman BK;
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                        (INCY-) INCYTE GENOMICS INC.
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                                                                         Lalgudi RV, Ito LY,
                                                                                                                           WPI; 2003-208840/20.
                                                                                                                                                                                                                                                      development.
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1191 ITTICITICACTCGAGATGCGGTGAGAGCAGGCTACGTGCAGTGTACAAGAAGTACTCGAA 1250
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                            831 gerraacgarcregrerereregacaargerracagregagagagarreregrear
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                                                                                                     GGAAAAGTTGATTCTGAACACGCTGCAGTTCAACATGTCTGTTCCAACACCTTATGTCTT
                                                                                                                                                                  GGAGAAGGCAATTCTTGGAAACCTCGAATGGTATTTGACAGTCCCGACTCAATACGTCTT
                                                                                                                                                                                                                                       CATGAAGAGGTTTCTGAAAGCTGCAGATGCAGATAAACAGCTTGAGCTAGCGTCATTTTT
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                                                                                                                                                                                                                                                                                                                                                                         CATGCTGGAGCTCTGCTAGAATACCAAATGCTGAATTATCGGCCTTCGCATCTGGC
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cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
cotton; rice; barley; millet; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1296 CTACAAGTTCGGTTGCGTGGCCAAGATTTTGCCTGCGCAGTTCCTGCTG 1344
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Claim 1; Page 97-99; 122pp; English.
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P-PSDB; AAB35799.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to identifying a stress condition to which a plant replaced, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile-of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing pith increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                        Arabidopsis thaliana; plant; gene; stress; transgenic; ds
                                           stress regulated gene SEQ
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                                         Arabidopsis thaliana
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                                          GCTGGAACCAGTAAGCTCACTGGCGTGCACAGAAGTACAGTACCTACAAGTTCGGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 34857.
                                                                                                                                                                                                                                                                                               AAC42253 standard; DNA; 1385 BP.
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9905-0126785P.
9905-0128244P.
9905-0128714P.
9905-012845P.
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29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
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          care useful for producing transgenic plants such as maize, soybean, surflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and millower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and cativity to forgium and cyclin-dependent kinases. The DNA sequences are also useful as probes for detecting deficiencies in the lavel of mRNA in screening for desired transgenic plants, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detecting any number of allelic variants, orthologs or paralogs of the gene, and site-directed mutagenesis in eukaryotic cells. The DNA sequences are also useful for recombinant expression of the encoded polypeptides and as immunogens for preparaing and screening antibodies. A transgenic plant comprising an expression cassette including a cell cycle regulatory gene is useful for assaying enzyme agonists and antagonists, and as immunogens or antigens to obtain antibodies. The antibodies are useful in essaying enzyme agonists and antagonists, for identifying and isolating nucleic acids from other species, and for purification of the proteins or an objective control of the proteins.
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cycle polynucleotides. The cell cycle polynucleotide sequences
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al Similarity 54.9%; Pred. No. 1.8e-41;
464; Conservative 0; Mismatches 360; Indels 2:
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Score 191.8; DB 3; Length 1385; Pred. No. 3.6e-40;

11.7%; 55.4%;

Query Match Best Local Similarity us-09-496-444-1.rng

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dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
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                                                                                                                    Homo sapiens.
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                               536 TCATGGATATTGACAGTGCAGACTCGGGGAACCCGCTTGCTGCAACAGAATATGTTAAAG 595
                                                                 559 TGATCGACATTGATGCTGTGGATGCTAACAATGAACTGGCTGCTGCAGAATACGTAGAGG 618
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AACTIOT to AACT8448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and calls the genes are expressed in. Example of activities conclude: cytostatic; proliferative; vulnerary; immunomodulator; conclude: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; antidabetic; conclude: cytostropic; antipsoriatic and antianglogenic. The nootropic; vasotropic; antipsoriatic and antianglogenic. The notropic; vasotropic; antipsoriatic and antianglogenic. The polymolectides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Collymolectides, polypeptides, antibodies, agoniets and antagonists from the proliferation, differentiation or mobilisation of immune cells, to traat disorders of haematopoietic cells, autoimmune cells, to traat disorders of haematopoietic cells, autoimmune cells. Inflammation, cancers, cardiovascular disorders, neuclodies and disease and creatial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of the breaser invarian
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Pred. No. 4.4e-32;
1; Mismatches 257; Indels 3;
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26-SEP-2003
                                                                                                                                                                                        Query Match
Best Local Sim:
Matches 328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polymucleotides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                         TATCTGACCGTGCCTACACAAAGGGCAAATTTTAGAAATGGAAAAGTTGATTCTGAACA
                                                                                                                                    956 CGCTGCAGTTCAACATGTCTGTTCCAACACCTTATGTCTTCATGAAGAGGTTTCTGAAAG
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                                                                                                                                                                                CTGCAGATGCAGATAAACAGCTTGAGCTAGCGTCATTTTTTCATGCTGGAGCTCTGGCTTGG
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                       GATTTTTACAGGTTCAGCCAGTTTCCCGGAAGAAGCTTCAATTAGTTGGGATTACTGGTC
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Otsuki
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A, Nagai K,
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T, Wakamatsu
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27-ANG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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Sugiyama
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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least less that the comprises at least libraries and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the fill-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13632 to AAH13632 to AAH13632 represent human amino acid sequences; and AAH13622 represent coligonucleotides, all of which are used in the exemplification of the
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Pred. No. 9e-32;
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536 TCATGGATATTGACAGTGCAGACTCGGGGAACCCGGCTTGCTGCAACAGAATATGTTAAAG
               TAGAATACCAAATGCTGAATTATCGGCCTTCGCATCTGGCTGCTGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a combination comprising cDNAs or their complements that are differentially expressed in respiratory disorder. The combination is useful for preparing a composition for diagnosing or treating respiratory disorders e.g. lung cancer, chronic obstructive pulmonary disease, emphysema or asthma. The present sequence represents human cDNA differentially expressed during lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rccachccaachtragchrordcagadachcroranargegergegarraggarc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 TCATGGATATTGACAGTGCAGACTCGGGGAACCCGCTTGCTGCAACAGAATATGTTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New combination comprising cDNAs that are differentially expressed in dispiratory disorders, useful for diagnosing or treating respiratory disorders e.g., lung cancer, chronic obstructive pulmonary disease, emphysema or asthma.
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Pred. No. 9.1e-32;
0; Mismatches 258; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1532 BP; 433 A; 350 C; 347 G; 402 T; 0 U; 0 Other;
respiratory disorder; lung cancer; asthma; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page; 39pp; English.
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                                                                                                                                                                                                                                04-APR-2002; 2002US-00116802.
                                                                                                                                                                                                                                                                                   04-APR-2001; 2001US-0281593P
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328; Conservative
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                                                                                                                                                                                                                                                                                                                                             (LASE/) LASEK A W.
                                                                                                                   US2003065157-A1
                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                   Lasek AW;
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The present sequence encodes a human cyclin related protein (HCRP)
designated HCRP-2 HCRP proteins can be used to treat cancer e.g.
denocarcinoma, leuksemia, etc. or immune disorders e.g. tabb, asthma.

They can also be used to treat developmental disorders, e.g. renal
tubular acidosis, cerebral palsy HCRP-2 was expressed in cancerous and
total tissues, and increased expression was proposed to be associated
with cancer and decreased expression with developmental disorders. HCRP
with cancer and decreased expression with developmental disorders. HCRP
can be used to screen for agonists (useful to treat conditions as above)
or antagonists. It can be used to generate antibodies, useful as
antagonists or to diagnose conditions characterised by HCRP expression
and to monitor therapeutic interventions. Polynuclectides encoding HCRP
can be used to detect polynuclectides encoding HCRP, e.g. to diagnose
diseases relating to polypeptide expression or monitor HCRP regulation
diseases relating to polypeptide expression or monitor HCRP regulation
of units pherapeutic intervention. They are useful to produce complementary
or antisense sequences for therapeutic administration to modulate or
control HCRP expression e.g. to treat or prevent cancers as above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ť.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cyclin related protein; HCRP; HCRP-2; cancer; adenocarcinoma; leukaemia; immune disorder; AIDS; asthma; developmental disorder; renal tubular acidosis; cerebral palsy; ss.
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9.8%; Score 160.2; DB 2; Length 1981;
Best Local Similarity 55.7%; Pred. No. 1e-31;
Matches 328; Conservative 0; Mismatches 258; Indels 3;
          1103
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1055 reciacrarcararecrecarrarecrireralegraceacacacide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding a cyclin related protein HCRP-2.
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WPI; 2000-617338/59.
P-PSDB; AAU78105.
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                                                                                                                                                                                                                                     This invention relates to a novel method for cloning and preparing human cyclin B2, the invention comprises CDNA and protein sequences for human cyclin B2 and reverse transcriptase (RT-) FOR primer sequences for human polylinker sequences that may be used in the cloning method. The invention also comprises a method for generation of an anti-cyclin B2 antibody and methods for its use. The present sequence represents the human cyclin B2 cDNA sequence of the invention
Process for preparing human cycline B2 gene cloning and anti-cycline B2 antibody, and usage thereof.
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9.7%; Score 158.6; DB 3; Length 1401;
Best Local Similarity 55.5%; Pred. No. 2.3e-31;
Matches 327; Conservative 0; Mismatches 259; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rcaacharganardegracanharcancchrchaaggradcagcagchac 954
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                                                                                                                                                   Claim 1; Page 6; 14pp; English.
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orditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a genes (1) in a test sample or determining the expression profile of a genes group in the sample comprising genes selected from (1). The method is useful for examining the ischaemia condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or indicator who screening for ischaemic condition-improving drugs or primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                          Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                    disease; ss
Mouse, ischaemia, compressive ischaemia, occlusive isc
vasospastic ischaemia, ischaemic condition, ischaemic
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Sequence 2308 BP; 631 A; 499 C; 517 G; 661 T; 0 U; 0 Other;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 21, Application US/10083889

Batent No. 6673894

GENERAL INFORMATION:
APPLICANT: Zahner, Joseph E.

TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.

FILE REFERENCE: 16850-7331

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: US/10/083,889

PRIOR APPLICATION NUMBER: US 60/271,798

PRIOR FILING DATE: 2001-02-27

NUMBER OF SEQ ID NOS: 25
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APPLICANT: Zahner, Joseph E.
TITLE OF INVENTION: Inhibitor of cell proliferation and methods of use thereof.
FILE REFERENCE: 16850-7331
CURRENT APPLICATION NUMBER: US/10/083,889
CURRENT FILING DATE: 2002-02-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1065 rodacrargarardergearrarearecricaraggaggagerge 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 1375;
                                                                                                                                                                                                                                                                                                                                                                                                                     9.8%; Score 160.2; DB 4; Length 55.7%; Pred. No. 1.6e-34; tive 0; Mismatches 258; Indels
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Patent No. 6673894
                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word 97
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 55.77
Matches 328, Conservative
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                          1375
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956 CGCTGCAGTTCAACATGTCTGTTCCAACACCTTATGTCTTCATGAAGAGGGTTTCTGAAAG 1015
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) DATABASE ENTRY DATE: 2000-11-01
US-10-083-889-1
                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Liu, J.H.
AUTHORS: Mei, S.
AUTHORS: Burnette, P.K.
AUTHORS: Gamero, A.M.
AUTHORS: Gunero, M.M.
AUTHORS: Gunero, J.Y.
AUTHORS: Didut, J.Y.
TITLE: Functional association of TGF-beta receptor II with cyclin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n 9.8%; Score 160.2; DB 4; Length 1530; Similarity 55.7%; Pred. No. 1.7e-34; 28; Conservative 0; Mismatches 258; Indels 3;
PRIOR APPLICATION NUMBER: US 60/271,798
PRIOR FILING DATE: 2001-02-27
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Word 97
SEQ ID NO 1
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Matches 328; Conservative
                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
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US-08-187-785-2
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956 CGCTGCAGTTCAACATGTCTGTTCCAACACCTTATGTCTTCATGAAGAGGTTTCTGAAAG 1015
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                                                                 844 idrinairdeaageaahaiaidaagaaarigiacceiceagaaridgagacringe 903
836 TGCTGCTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGA 895
                                                                                                                                               896 TATCTGACCGTGCCTACACAAAGGGCAAATTTTAGAAATGGAAAAGTTGATTCTGAACA
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
FULLING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETI
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1048, Application US/09023655
; Patent No. 6607879
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: singl
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| IMMEDIATE SOURCE:
| LIBRARY: GENBANK
| CLONE: 9181243
| US-09-023-655-1048
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                                                  GENERAL INFORMATION:
APPLICANT: Epstein, Stephen
APPLICANT: Dager, Ellis
APPLICANT: Unger, Ellis
APPLICANT: Unger, Ellis
APPLICANT: Unger, Ellis
TITLE OF INVENTION: Inhibition of No. 5756476-Transformed Cell
TITLE OF INVENTION: Proliferation Using Anti-Sense Oligonucleotides
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSES: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STREET: GA
STREET: 0AA
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STREET: 0AA
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,415
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/187,785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIHO;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
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-INDIVIDUAL ISOLATE: Human
IMMEDIATE SOURCE:
CLONE: CYCLIN B1 CDNA clone
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EDNESS: single
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US-08-187-785-2
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      DB 4; Length 1452;
Query Match
9.5%; Score 155.4; DB 4; Length 1
Best Local Similarity 54.7%; Pred. No. 3.6e-33;
Matches 331; Conservative 0; Mismatches 271; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Boston
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                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,299A
FILING DATE: 20-APR-1995
                                                                                                                                                                                                                                                                                                                     NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: HMI-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1302 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                       FILING DATE: 20-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
SOFTWARE: ASCII (text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 7.7%; Score 125.6; DB 2; Length Local Similarity 52.2%; Pred. No. 7.7e-25; Length 52.8; Conservative 0; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAMERICAY: Human cyclin A LOCATION: coding sequence from base 97 to base 1392, LOCATION: coding for a protein of 432 amino acids.
                                                                                                                                                                WEDIUM TYPE: Diskette-5.25 inch, 500 Kb storage COMPUTER: IBM PC/XT/AT or compatibles COMPUTER: IBM PC/XT/AT or compatibles opeRATING SYSTEM: MS-DOS version 3.0 or above SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/460,895 FILING DATE: 05-UNN-1995 CLASSIFICATION DATA: APPLICATION NUMBER: 07/650, 805 FILING DATE: 06-FEB-1991 APPLICATION NUMBER: FF9001596 FILING DATE: 12-FEB-1990 INPORMATION POR SEQ ID NO: 1 : SEQUENCE CHARRACTERISTICS: LENGTH: 1634 base pairs
                     3: Larson and Taylor
727 Twenty-Third Street, South
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                              Arlington
Virginia
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; LOCATION:
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US-08-460-895-1
                                                              CITY: Ar
STATE: V
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Best Local S:
Matches 328
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Sequence 1, Application US/08460895

Setent No. 5849508

GENERAL INFORMATION:
   APPLICANT: BRECHOT,
   APPLICANT: WANG, Jian
   APPLICANT: CHENIVESSE, Xavier
   APPLICANT: HENGLEIN, Berthold
   APPLICANT: HENGLEIN, Berthold
   APPLICANT: TINDY, Fr d rique
   TITLE OF INVENTION: NEW HUMAN CYCLIN A COMPOSITIONS AND A PROCESS FOR THEIR PRODUC
   NUMBER OF SEQUENCES: 1
                                                                                                                                      use thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                   Sequence 25, Application US/10083889

Patent No. 6673894

GENERAL INFORMATION:

APPLICANT: Zahner, Joseph E.

TITLE OF INVENTION: Inhibitor of cell proliferation and methods of user present APPLICATION NUMBER: US/10/083,889

CURRENT APPLICATION NUMBER: US 60/271,798

PRIOR PILING DATE: 2001-02-27

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Mcrosoft Word 97

LENGTH: 1336
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Pred. No. 2.4e-29;
0; Mismatches 229; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.7%;
Matches 292; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus US-10-083-889-25
                               10-083-889-25
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US-08-460-895-1
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                                                                                                                                                                                                                                                                                                                                                                                                                 931 digracairacadargaraccracdacdagaaacaadagircrgagaardagagcarcragir 990
                                                                                                                                                                                                                                                                                                                              871 GCTGCTATGCTGTTAGCCTCAAAGTTTGAAGAAATATACCCCCCAGAAGTAGCAGAGTTT 930
                                                                                                                                                                                                                                                                                                                                                                        GIGCTGATATCTGACCGIGCCTACAAAAGGGCAAATTTTAGAAATGGAAAAGTTGATT 948
                                                                                                                        709 ATTGAGGITCACTACAAGITTGAACTGATGAAGACGCTCTTTCTTATGGTAAACATA 768
                                                                                                                                                              751 GİTGAAĞTAGGAGAAÇAATATAAĞTACAĞAATĞAĞAÇÇÇTGCATTTGGCTĞTĞAĞCTAC 810
                                                                                                                                                                                                        ATAGATAGATTCTTGGAAAAGGAAGTGGTTCCAAGGAAGAAGAAGTACAACTGGTTGGAGTC 828
                                                                                                                                                                                                                                                811 Africkárkósírtetretretretrekársársakákakárteksérrékséretreksőkeren 870
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631 CATGAGGATATTCACACATACCTTAGGGAAATGGAGGTTAAATGTAAACCTAAAGTGGGT
                                                                                  691 TACATGAAGAACAGCCAGACATCACTAACAGTATGAGAGCTATCCTCGTGGACTGGTTA
                                                                                                                                                                                                                                                                                          829 ACAGCTATGCTGCTCGCTTGTAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTT
                                            TACATGTCCAGCCAACAAGACATAAACTCAAAGATGAGAGCAATTCTGATTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08692787;
Sequence 8, Application US/08692787;
Patent No. 5882864
GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: Ralph, David
APPLICANT: Veltri, Robert
TITLE OF INVENTION: BIOWARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/692,787
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
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NAME: Corder, Tinothy S.
REGISTRATION NUMBER: 38,414
REFERENCE/DOCKET NUMBER: UDC:012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Texas
COUNTRY: United States of America
ZIP: 77210
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Sequence 1, Application US/09210889

GENERAL INFORMATION:
APPLICANT: RRECHOT, Christian
APPLICANT: WANG, Jian
APPLICANT: CHENIVESSE, Xavier
APPLICANT: TINDY, Fd frique
TITLE OF INVENTION: FG FROM FROM FROM FROM THE CORRESPONDING NUCLEOTIDE SEG
TITLE OF INVENTION: A PROCESS FOR THEIR PRODUCTION, THE CORRESPONDING NUCLEOTIDE SEG
TITLE OF INVENTION: A PROCESS AND AGENTS FOR CELL PROLIFERATION OR DIAGN
TITLE OF SEQUENCES:
UNDERREPONDENCE ADDRESS:
                                                                         1122
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               529 GAATTGCTCATGGATATTGACAGTGCAGACTCGGGGAACCCGCTTGCTGCAACAGAATAT 588
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                                                                         1066 CTCTGCTTGGTAGAAT---ACCAAATGCTGAATTATCGGCCTTCGCATCTGGCTGCTGCT
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727 Twenty-Third Street, South
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APPLICATION NUMBER: 07/650, 805
FILING DATE: 06-PEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC/XT/AT or con OPPERATING SYSTEM: MS-DOS VETS SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION NUMBER: US/09/21 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-FEB-1990
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: single
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ORIGINAL SOURCE
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FEATURE:
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LOCATION:
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COUNTRY:
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US-09-210-889-1
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Version #1.30

YSTEM: PC-DOS/MS-DOS PatentIn Release #1.0,

IBM PC compatible

Box 4433

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FILING DATE:
CLASSIFICATION:
PRIOR PEDICATION DATA:
APPLICATION NUMBER: US 08/692,787
FILING DATE: 31-UTL-199:
ATTORNEY/AGENT INFORMATION:
NAME: NAKASHİMA, RİCHARA A.
                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,199
                                                                                                                                                                                                                                                                                                                          NAME: Nakashima, Richard A. REGISTRATION NUMBER: P-42,023
                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: U
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
                                                                                              COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                    OPERATING SYSTEM:
STREET: F.v.
                    CITY: L. STATE: Texas COUNTRY: USA
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                                                                                                                                                                                          Length 1649;
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                                                                                                                                                                                        Score 125.6; DB 2;
Pred. No. 7.7e-25;
0; Mismatches 294;
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                            TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                (512) 418-3000
                                                  œ
                                                                                                                                                                                        Query Match
Best Local Similarity 52.2%;
Matches 328; Conservative
                                                                                                                                     TOPOLOGY: linear
                  TELEPHONE:
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                                                                                                                                                                         Gaps
                                                                                                                                                                    9
                                                                                                                       Length 1649;
                                                                                                                                                                         Indels
                                                                                                                       Score 125.6; DB 3;
Pred. No. 7.7e-25;
0; Mismatches 294;
                                                                                                                          Query Match
Best Local Similarity 52.2%;
Matches 328; Conservative
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                      TOPOLOGY:
US-09-097-199-8
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DISEASE

Sequence 8, Application US/09097199;
Patent No. 6218529;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: An, Gang
APPLICANT: Ralph, David
APPLICANT: Ralph, David
APPLICANT: Ralph, David
APPLICANT: Ralph, David
TITLE OF INVENTION: BIOWARKERS AND TARGETS FOR DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND MANAGEMENT OF PROSTATE DISE;
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

RESULT 11 US-09-097-199-8

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1006 ȚITCIGAAAGCIGCAGAIGCAGAIAAAACAGCIIGAGCIAGCGICAIȚITȚCAIGCIGGAG 1065
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                                                                                                                                                   822 ATTGATAGGTTCCTCCTTCCATGTCAGTGCTGAGAGAAAACTTCAGCTTGTGGGCACT 881
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        762 GTTGAAGTAGGAGAAGAATATAAACTACAGAATGAGACCCTGCATTTGGCTGTGAACTAC 821
                                                                                                        769 ATAGATAGATTCTTGGAAAAGGAAGTTCCCAAGGAAGAAGCTACAACTGGTTGGAGTC 828
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APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
APPLICANT: Damagnez, Veronique
APPLICANT: Damagnez, Veronique
APPLICANT: Drawetta, Guilio
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
TITLE OF INVENTION: Human Pathogens, and Uses Related Thereto
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1123 GCGGTTTATACTGCACAGTGTGCTATCA 1150
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,090B
FILING DATE: 05-UIM-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Foley, Hoag & Eliot, LLP
One Post Office Square
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NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIVOS
TELEPHONE: (617) 832-1299
TELEPHONE: (617) 832-1299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1752 base pairs
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STRANDEDNESS: both
TOPOLOGY: linear
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STREET: CLLC
TTV: Boston
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ZIP: 02109
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1122 TIAAGTITGATAGAIGCTGACCCAIACCTCCAGTATTIGCCATCAGTIATITGCTGGAGCT 1181
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                                                                                                                                                                                                                                           Sequence 1268, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G Stuart
APPLICANT: Susan G Stuart
APPLICANT: GENERAL OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                          1123 GCGGTTTATACTGCACAGTGTGCTATCA 1150
                                                                                                                        1182 GCCTTTCATTAGCACTCTACACAGTCA 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 94-0001 US
TELECOMMUNICATION INPORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION POR SEQ ID NO: 1268:
SEQUENCE CHARACTERISTICS:
LENGTH: 1649 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
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STRANDEDNESS: single
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CLASSIFICATION:
PRIOR APPLICATION DATA;
APPLICATION NUMBER:
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: CALIFORNIA
RY: USA
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US-09-023-655-1268
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STATE: CA
, COUNTRY:
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AACAIGTCTGTTCCAACACCTTATGTCTTCATGAAGAGGTTTCTGAAAGCTGCAGATGCA 1026
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                                                                                                                    grrckgccaditrcccddaadaadacrrcaarradriddaatracrccadrcrdcrcriddcc
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                                                                                  AAGGAAGTGGTTCCAAGGAAGAAGCTACAACTGGTTGGAGTCACAGCTATGCTGCTCGCT
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TTTGAACTGATGGATGAGACGCTCTTTCTTATGGTAAACATAATAGATACATTGGAA
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6.8%; Score 111.6; DB 4;
Best Local Similarity 55.0%; Pred. No. 4.1e-21;
Matches 219; Conservative 0; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
(US-09-773-459-12)
(Sequence 12, Application US/09773459)
(Sequence 12, Application US/09773459)
(SERENAL INFORMATION:
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(SERENAL INFORMATION:
(SURENT RELING DATE: 1099-06-21)
(SURENT FILING DATE: 1999-06-21)
(SOFTWARE: FRASESQ for Windows Version 3.0)
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-773-459-12
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                                                                                                                                 7.3%; Score 119.6; DB 1; Length ilarity 50.0%; Pred. No. 3.7e-23; Conservative 0; Mismatches 299; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kennedy, Giulia C
APPLICANT: Kennedy, Giulia C
TITLE OF INVENTION: PANNERATIC CANCER GENES
FILE REFERENCE: 200130.454
CURRENT APPLICATION WUMBER: US/09/337,171
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 926
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; Sequence 12, Application US/09337171
; Patent No. 6262249
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184..1659
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ORGANISM: Homo sapien
                                                                                                                                   Query Match
Best Local Similarity
Matches 299; Conserv
           MOLECULE TYPE:
FEATURE:
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                                                     NAME/KEY:
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LOCATION:
US-08-463-090B-4
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Sequence 52554, A Sequence 13500, A Sequence 27403, A Sequence 109, App Sequence 26031, A Sequence 26031, A

Sequence 246 Sequence 345, Sequence 8,

Scoring table: Perfect score:

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Sequence:

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Sequence 1, Application US/09496444

| Sequence 1, Application US/09496444
| Publication No. US20030041343A1
| GENERAL INFORMATION:
| APPLICANT: Tao, Yumin
| APPLICANT: Dowe, Keith S.
| APPLICANT: Dowe, Keith S.
| APPLICANT: Bailey, Matthew A.
| TITLE OF INVENTION: Cell Cycle Polynucleotide, Polypeptide, TITLE OF INVENTION: and Uses Thereof FILE REFERENCE: 1109
| CURRENT APPLICATION NUMBER: US/09/496,444
| CURRENT FILING DATE: 2000-02-02
| FARLIER APPLICATION NUMBER: US 60/119,857
| SARLIER FILING DATE: 1999-02-12
| SARLIER FILING DATE: 1999-02-103
| SARLIER FILING DATE: 1999-02-103
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2 US-10-425-11-7906
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US-09-925-301-305
US-09-954-456-695
US-09-954-456-695
US-09-967-133
US-09-967-168A-145
US-09-967-168A-145
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US-10-108-605-246
US-09-925-300-345
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; OTHER INFORMATION: n = A,T,C or
US-09-496-444-1
                                                                                                           (109)...(1381)
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LOCATION: (109)...(1381
NAME/KEY: misc feature
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ORGANISM: Zea mays
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Sequence 46, Appl
Sequence 4753, Ap
Sequence 61, Appl
Sequence 51, Appl
Sequence 51, Appl
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Sequence 51, Appl
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118855,
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Sequence 789, App
Sequence 52, Appl
                                                                                                                                                                                                     March 20, 2004, 19:50:55 ; Search time 585 Seconds (without alignments) 10344.983 Million cell updates/sec
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1. (cgn2_6/prodata/// pubpna/USOT PUBCOMB.seq:*

3. (cgn2_6/prodata/// pubpna/USOG FUBF PUB.seq:*

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                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-310-154-50

US-10-310-154-46

US-10-310-154-46

US-10-310-154-61

US-10-310-154-61

US-10-260-238-4753

US-10-260-238-4753

US-10-260-238-4753

US-10-260-238-1251

US-10-424-599-118855

US-10-60-238-1251

US-10-60-238-1251

US-10-60-238-1251

US-10-60-238-1251

US-09-938-842A-789

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US-09-938-842A-789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2438257 seqs, 1849576744 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                  nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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Result No.

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CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
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    Luethy, Michael M.
Lund, Adrian
Madson, Linda L.
Malloy, Kathleen A.
Malloy, Kathleen A.
Miler, Philip W.
Padmavathi, Manchikanti
Parnell, Laurence D.
Start, William G.
Tennesen, Dan
Vidya, K.R.
Wang, Haiyun
Xin, Zhanguo
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Best Local Similarity 99.0%;
Matches 1619; Conservative
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Zhao, Yajuan
Zhou, Li
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1589 IGCTIGIGCAGTIATACIGCGGCTAAIAACAAACIGICCAGITATICIAAAAAAACAACGA 1648
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TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REPRENCE: 38-15(5796) B
CURRENT APPLICAN NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Madson, Linda L.
Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
Parnell, Laurence D.
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PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 46
LENGTH: 1611
                                                                                                    Sequence 46, Application US/10310154
Publication No. US20030233670A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
                                                                                                                                                                                                                                                                                                                                                               Kretzmer, Keith A
Laccetti, Lucille B.
Lai, Chao-Qiang
Lee, Gary
                                                                                                                                                                                    Agarwal, Ameeta K.
Ahrens, Jeffrey E.
Ball, James A.
Banu, G.
Bell, Erin
Boddualli, Raghava
Deikman, Jil
Deng, Molian
Dong, Jinzhuo
Duff, Stephen M.
Galligan, Meghan M.
Hinchey, Brenda S.
Hinchey, Brenda S.
Huang, Shihshieh
Jung, Vincent
                       AAAAAAAAAAAAA 1636
                                              1649 ACGATGTTCAGGAAAA 1664
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Tennesen, Dan
Vidya, K.R.
Wang, Halyun
Xin, Zhanguo
Xu, Nanfel
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Zeng, Xiaoping
Zhang, Qiang
Zhao, Yajuan
Zhou, Li
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Lund, Adrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | FEATURE:
| NAME/KEY: CDS
| LOCATION: (74)..(1336)
| OTHER INFORMATION:
| US-10-310-154-46
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ORGANISM: Oryza sativa
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1008 TCTGAAAGCTGCAGATGCAGATAAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCT 1067
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                                                                                                                                                                                                                                                                                                                                                                                                                       174 AGACATGGCGAGCGGGGGGGCGCTCACGACATCAAGAACCTCGTCGGGGCTGCCCGTA 233
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                                                                                                        29;
Length 1611;
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Score 702.2; DB 15;
Pred. No. 4.2e-200;
0; Mismatches 323;
Query Match
Best Local Similarity 73.3%;
Matches 965; Conservative
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1186 İGCACCATTAATGGGTTCAAĞTCCTGGAACAAATGCTGTGAGCTGCATACAAAATACTCT 1245
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CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 44
LENGTH: 1793
                                                                                                                                                                                                                                                                     24.5%;
al Similarity 68.5%;
553; Conservative
                                                                                                                                           NAME/KEY: CDS
LOCATION: (148)..(1407)
OTHER INFORMATION:
                                                                                                   TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 553
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                                                                                     GAAGGCTGGAACCAGTAAGCTCACTGGCGTGCACAGGAAGTACAGTACCTACAAGTTCGG 1307
                                                                                                                                                                        TIGGGIGGCCAAGATITITGCCIGGGCAGITCCIGGIGGAGICGGGAG--GGACACCGCCT 1365
                                                                                                                                                                                          CCTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTGGATTTTTAAAGTT 1422
                                                                                                                                                                                                                                                        CCTTCAGAAGCAGCCTTGTTGAATGAATCTATTCCCCTGGATAGATTTTTTAACTT 1371
      TTATACTGCACAGTGTGCTATCAATCGTTGCCAGCACTGGACAAAGGTCTGCGAGTCTCCA
                              TTACACAGCACAATGTGCTCTCACTGGTTGCCAGCAGTGGACAAAGACCTGCGAACTACA
                                                            TAGCAGATACACTAGCGACCAACTCCTGGAGTGCTCGAGGATGATGGTAGATTTTCACCA
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APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
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Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
Parnell, Laurence D.
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Publication No. US20030233670A1
GENERAL INFORMATION:
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Laccetti, Lucille B.
Lai, Chao-Qiang
Lee, Gary
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Boddupalli, Raghava
Deikman, Jill
Deng, Molian
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APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Reff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
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Jung, Vincent
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Hinchey, Brenda S.
Huang, Shihshieh
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Start, William G.
Tennesen, Dan
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, Stephen M.
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Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
Yang, Chunzhi
Zeng, Xiaoping
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Liu, Jingdong
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Zhao, Yajuan
Zhou, Li
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946 GACCGCGCCTACACAAAAAACAGATATTCTCGAAATGGAGGATGATTGTAAACACTCTT 1005 CAGITCAACAIGICIGIICCAACACCTIAIGICIICAIGAAGAGGIIICIGAAAGCIGCA 1020 1021 GATGCAGATAAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTCTGCTTGGTAGAA 1080 646 TACAGCTTCTACAGGAGGAGGAGGGTTTGAGCTGTGTCTCTCCTAATTACATGTTGAGG. 705 CAACAAGACATAAACTCAAAGATGAGGAATTCTGATTGACTGGCTGATTGAGGTTCAC 720 706 caaaardacaraaargagaadargcgcgcarrcrccarcgarrggcrgaragagggggr 765 766 tacaagitagagctartiggargagacctictriccttactigaaratcatagaccgatic 825 TIGGAAAAGGAAGIGGIICCAAGGAAGAAGCIACAACIGGIIGGAGICACAGCIAIGCIG 840 |||||| Trggcrcgcgaaaatgrggrggaaagafgcrtcagtrggrrggcgrgacrgccargcrg 885 CTCGCTTGTAAATATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCT 900 886 criceccreciárica a caracida de controcrera de contratoria de contratoridos de contratoridos de contratoridos de contratoridos de contratoridos de contratoridos de contratoridos de contratorios de contra TACCAAATGCTGAATTATCGGCCTTCGCATCTGGCTGCTGCTGCTGTTATATACTGCACAG 601 TACACCTTTTACAGAGAAAATGAGGCTAAGAGTTGTGTAAAGGCCAGATTACATGTCCAGC GACCGTGCCTACACAAAAGGGCAAATTTTAGAAATGGAAAAGTTGATTCTGAACACGCTG 1006 CAGTITGATAIGICAGIICCAACICCAIACTGIITCAIGAGAAGGIICCICAAGGCIGCA targagariecteaarrecagecereaarecresegecrecreseareracaeresege 541 GATATTGACAGTGCAGACTCGGGGAACCCGCTTGCTGCAACAGAATATGTTAAAGAGCTT s86 garatricacagergreargeaaraacreecritecagragergaarargargargaarr Gaps Score 400.6; DB 15; Length 1793; Pred. No. 3.2e-109; O; Mismatches 254; Indels O; NAME/KEY: unsure | LOCATION: (1)..(1793) | OTHER INFORMATION: unsure at all n locations US-10-310-154-44

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ccciarideacaartrargarireaacaardaacaaaacardaaagaagaacaaarr 1342
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                                                        CACAGTGTGCTATCATCGTTGCCAGCACTGGACAAAGGTCTGCGAGTCTCATAGCAGAT
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TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
                    TAGAATACCAAATGCTGAATTATCGGCCTTCGCATCTGGCTGCTGCT
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Madeon, Linda L.
Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmayathl, Manchikanti
Parnell, Laurence D.
Start, William G.
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Publication No. US20030233670A1
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Kretzmer, Keith A
Laccetti, Lucille B.
Lai, Chao-Qiang
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Boddupalli, Raghava
Deikman, Jill
Deng, Molian
Dong, Jinzhuo
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Jung, Vincent
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Hinchey, Brenda S.
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Ball, James A.
Banu, G.
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Adams, Thomas H
Ruff, Thomas G.
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Vidya, K.R.
Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
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Zhao, Yajuan
Zhou, Li
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Lin, Jie-Yi
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1306 GGGAAGCTTACTGGAGTTCATAGAAAGTACAGCACATTTAGGTATGGTTGCCCCGCAAAA 1365
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APPLICANT: Kovalic David K
APPLICANT: Show Thomas J
APPLICANT: Show The Applicant: A construction of the Applicant: Can Yongwein
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules J
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(3323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 4553
FURNION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF THE APPLICATION OF T
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65.4%; Pred. No. 1.2e-105;
ive 0; Mismatches 302;
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                                                           1321 ATTTTGCCTGCGCAGTTCCTGCTGGAG 1347
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Sequence 4/753, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Matthes 570; Conservative
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Glazebrook, Jane
Goff, Stephen A.
Katagiri, Fumiyaki
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Best Local Similarity 67.8%;
Matches 556; Conservative
                                                                                                                                                                                               APPLICANT: Budworth, Paul R. APPLICANT: Moughamer, Todd G APPLICANT: Briggs, Steven P. APPLICANT: Cooper, Bret
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US-10-260-238-497
                                                                                                                                                                                                                                                                                                                                                              Kreps, Joel
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21.7%; Score 355.4; DB 15; Length
Best Local Similarity 64.8%; Pred. No. 1.3e-95;
Matches 527; Conservative 0; Mismatches 286; Indels
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FILE REFERENCE: 38-15(52796)B
CURRENY PEPLICATION NUMBER: US/10/310,154
CURRENY FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF EQ ID NOS: 736
SEQ ID NO 61
                                                                                                                                                                                                                                                                     ; LOCATION: (114)..(1385); OTHER INFORMATION:
US-10-310-154-61
                                                                                                                                                                               TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1116
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APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: ALL, Tong
TILLE OF INVENTION: PROWOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT APPLICATION NUMBER: US 60/325,448
PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 6077
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Pred. No. 8.7e-92;
0; Mismatches 251; Indels
1356 TCGGAACCCGCAACTTTCTTGCTGGATGCCTGA 1388
                                                                                                                                                                                                               Sequence 497, Application US/10260238 Publication No. US20040016025A1 GENERAL INFORMATION:
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1249 racecearecrecaritacecrecaredereacededededededererarecrecaed 1308
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                                      TITLE OF INVENTION:
FILE REPERENCE: 38-15(52796)B
FILE REPERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO S: 736
LENGTH: 1751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.9%; Score 243.8; DB 15; Length 56.0%; Pred. No. 5.5e-62; tive 0; Mismatches 362; Indels
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Best Local Similarity 56.0
Matches 461; Conservative
Zhao, Yajuan
Zhou, Li
                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: CDS
; LOCATION: (82)..(1518)
; OTHER INFORMATION:
US-10-310-154-51
                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Zea mays FEATURE:
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  1015 GCTGCAGATGCAGAT----AAACAGCTTGAGCTAGCGTCATTTTTCATGCTGGAGCTC 1068
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                                                                                                                                                                                                                                                                     1047 TACACTGCTCAGTGCACCATTAATGGGTTCAAGTCCTGGAACAAATGCTGTGAGCTGCAT
                                                                                                                                                                                                                      TATACTGCACAGTGTGCTATCATTCGTTGCCAGCACTGGACAAAGGTCTGCGAGTCTCAT
                                         TGCTTGGTAGAATACCAAATGCTGAATTATCGGCCTTCGCATCTGGCTGCTGCCGGTT
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Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmavathi, Manchikanti
Parnell, Laurence D.
Start, William G.
Tennesen, Dan
Vidya, K.R.
Wang, Haiyun
Xin, Zhanguo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/10310154; Publication No. US20030233670A1
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Duff, Stephen M.
Galligan, Meghan M.
Hinchey, Brenda S.
Huang, Shinshieh
Johnson, G. Richard
Jung, Vincent
Kretzmer, Keith A
Laccetti, Lucille B.
Lai, Chao-Qiang
Lee, Gary
Lin, Jie-Yi
Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bell, Erin
Boddupalli, Raghava
Deikman, Jill
Deng, Molian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chomet, Paul S. Adams, Thomas H. Ruff, Thomas G. Agarwal, Ameeta K. Ahrens, Jeffrey B. Ball, James A. Banu, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michael M.
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Zeng, Xiaoping
Zhang, Qiang
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Lund, Adrian
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1168 ACAAAGGTCTGCGAGTCTCATAGCAGATACACTAGCGACCAACTCCTGGAGTGCTCGAGG 1227
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                              1108 CATCTGGCTGCTGCTGCGGTTTATACTGCACAGTGTGCTATCAATCGTTGCCAGCACTGG 1167
                                                                                   567 ATGGTTGCTGAGCTGTGTTTGCAGCAAGATGCACTCTGAACAAGGCTCCCTTTGG 626
                                                                                                                                                                                               627 Aargagacacrraagcrgcacacrogrracrcacaagagcaacrcarggarrgrgcraga 686
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APPLICANT: Budwartch, Paul R.
APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Briggs, Stephen A.
APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Greps, Joel
APPLICANT: Karagiri, Fumiyaki
APPLICANT: Karagiri, Fumiyaki
APPLICANT: Karagiri, Fumiyaki
APPLICANT: Karagiri, Fumiyaki
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Browners FOR REGULATION OF PLANT EXPRESSION
ITILE OF INVENTION BROWOTERS FOR REGULATION OF PLANT
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PLILING DATE: 2001-09-26
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OTHER INFORMATION: n = any nucleotide
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LOCATION: (898)...(898)

OTHER INFORMATION: n = any nucleotide

US-10-260-238-1251
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OTHER INFORMATION: n =
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OTHER INFORMATION: n =
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ORGANISM: Oryza sativa
FEATURE:
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NAME/KEY: N region
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Publication No. US20040031072A1
CENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwai
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NOS: 285684
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1429 AGCAAGCAAAAGGCGGTGTACAGGAAGTACTCCAAGCCCCAAGCTCGGCTCCGTCGCCTT 1488
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                                                          1321 ATTITGCCIGCGCAGTICCIGCTGGAGTCGGGAGGGACACCGC 1363
                                                                                                               0; Mismatches 334; Indels
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COTHER INFORMATION: unsure at all n locations
FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT3847_78333C.1
US-10-424-599-118853
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442; Conservative
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NAME/KEY: unsure
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RESULT 12
US-10-424-599-118855
; Sequence 118855, Application US/10424599
                                                                                                                  Query Match
Best Local Similarity 56.9%;
Matches 466; Conservative
                                                                               ) OTHER INFORMATION: Clone ID: US-10-424-599-103481
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 103481
LENGTH: 1944
                                              TYPE: DNA
ORGANISM: Glycine
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Los Vinus
APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28
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-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING AND METHODS OF USE
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                                                                                      1300 AAGTICGGIIGCGIGGCCAAGAITTIGCCIGGGCAGTICCTGCIG 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 214.6; DB 9; Length
Pred. No. 2.8e-53;
0; Mismatches 374; Indels
                                                                                                                                      1428 cadaaggargergirgergereceeeeeeeeraarireiree
                                                                                                                                                                                                                                                       US-09-338-942A-7

US-09-358-942A-7

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Harper, Jeff

APPLICANT: ARABY, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE REFERENCE: SCRIP1300-3

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR PILING DATE: 2000-08-24

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

LENGTH: 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Arabidopsis thaliana
US-09-938-842A-789
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ilarity 54.5%;
Conservative
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                                                                                                                                                                                                                 RESULT 13
US-09-938-842A-789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 452; (
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vousic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFRENCE: 38 -21 (5323.8)
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38 -21 (5323.8)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1007
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Pred. No. 2e-53;
0; Mismatches 371; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_78335C.1
US-10-424-599-118855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.7%;
Matches 451; Conservative
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Glycine max
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CIGCGAGICTCATAGCAGATACACTAGCGACCAACTCCTGGAGTGCTCGAGGATGATGGT 1235
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                                                                                                                                     gditaacdarchedigaagteacddacaardctraacagacagacagatrciegrear 890
                                                                                                                                                                                                                        891 dakakadecakircingakaccicakaheeningkacadicceakircankediri 950
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                                                                                                                                                                                                                                                                                                                                                          CATGCTGGAGCTCTGGTAGAATACCAAATGCTGAATTATCGGCCTTCGCATCTGGC
             ACTEGITEGAGICACAGCTATGCTGCTCGCTTGTAAATATAAGAGGAGGTATCTGTTCCAGT
                                                     771 géradraddarichardécridétratracricchahrhdhadharreraecenétren
                                                                                                876 TGTTGAGGACCTTGTGCTGATATCTGACCGTGCCTACACAAAAGGGCCAAATTTTAGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 52, Application US/10310154 Publication No. US20030233670A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galligan, Meghan M.
Hinchey, Brenda S.
Huang, Shihshieh
Johnson, G. Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Ball, James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boddupalli, Raghava
Deikman, Jill
Deng, Molian
Dong, Jinzhuo
Duff, Stephen M.
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Lund, Adrian
Madson, Linda L.
Malloy, Kathleen A.
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Kretzmer, Keith A
Laccetti, Lucille B.
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iu, Jingdong
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Bin
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publication No. US20040009476A9

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publication No. US20040009476A9

publication No. US20040009476A9

publicant: Kreps, Joeff

**, APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Son, STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

: TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-06-22

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: S379

SEQ ID NO 789

LENGTH: 1338
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                                              CATGCTGGAGCTCTGCTTGGTAGAATACCAAATGCTGAATTATCGGCCTTCGCATCTGGC
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US-09-,938-842A-789
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Best Local Similarity 56.6%; Pred. No. 1.2e-52;
Matches 466; Conservative 0; Mismatches 337; Indels 21; Gaps
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APPLICANT: Zhang, Qiang
APPLICANT: Zhang, Yajuan
APPLICANT: Zhao, Yajuan
APPLICANT: Zhao, Yajuan
APPLICANT: Zhao, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REPRENCE: 38-15(52796)B
CURRENT PILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 52
LENGTH: 1850
                   Miller, Philip W.
Padmavathi, Manchikanti
Parnell, Laurence D.
Start, William G.
McKiel, Christine L.
                                                                                              Tennesen, Dan
Vidya, K.R.
Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
                                                                                                                                                                                                 Yang, Chunzhi
Zeng, Xiaoping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ), NAME/KEY: CDS
; LOCATION: (254)..(1579)
; OTHER INFORMATION:
US-10-310-154-52
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ORGANISM: Zea mays
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Db 1284 TCGCTGAATTGGCGCTGATGACGATTTGGTGACACGCCTGCCATCGCTGGTCGCTG 1343

Qy 1118 CTGCTGCGCTTATACTGCACACGTGTCACACGCCTGCCACTGGTCGCTGCTGT 1177

Db 1134 CTTCTGCTGTCTCTACACGACCAGACTCCTTTGGACTGCACACGCCT 1103

Qy 11232 TGGTAGATTTTCACCACAGAGACTCAGAGAGACTCATTGAATGCTCGAGAAGAT 1231

Db 1404 TCAAGCACCACAGGGCTTCAGAAGATCAGAGAGACACCCT463

Qy 1232 TGGTAGATTTTCACCACAAGAGACAGAAGATCATGAATGCACAGAAGATGC 1463

Qy 1232 TGGTAGATTTTCACCACAAGAGACCAGAAGATCATGAATGCACAGAAGATTC 1523

Qy 1232 TGGTAGATTTCACCACAAGACCAGAAGATTATACACAGAAGATT 1523

Qy 1232 TGGTAGATTCGCACACGCCAAGAATTTTGCCTGGAGATTATACAAGAAGAATT 1523

Qy 1232 GTACCTACAAGATCGGTGGCCAAGATTTTGCCTGGAGAGTTATAAAAGAAGAATT 1523

Qy 1232 GTACCTACAAGTTCGAGAGGCCAACATTTTGCCTGGCGCAG 1335

Db 1524 CCAGCGACACGCCCCCCACACACTTTTGCCTGCCACAGA 1567

Search completed: March 20, 2004, 23:16:41
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March 20, 2004, 19:33:10 ; Search time 4447 Seconds (without alignments) 10985.952 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                         CGCCTCCTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTG--GATTTTTTAA
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Unpublished (1999)
Contact: Walbot (1999)
Contact: Walbot (1999)
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
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Fax: 650 725 8221
Fax: 650 725 8221
Lamil: Walbot@stanford.edu
Plate: 3529_1104 1 row: D column: 01.
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Walbot, V.
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| / organism="Saccharum officinarum" |
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| db xref="taxon:4547" |
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| / dab nost="bH108" |
| / dab nost="corgan: Inflorescence at begining of development (lorn-long); Vector: pSport1; Site=1: Sal1; Site=2: NotI; An unidirectional cDNA library generated from [Inflorescence at begining of development (lorn-long)].
| cDNA was prepared from polyah mRNA using SuperSorribt Plasmid System KIt (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0; 8 and 1.5 KD were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum.
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S Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. Tettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Contact: Arruda P
Contro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be through the Brazilian Clone distribution clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: COB row: F column: 11
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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36.6%; Score 598.8; DB 14; Length
Best Local Similarity 92.2%; Pred. No. 2.9e-80;
Matches 642; Conservative 0; Mismatches 52; Indels
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GATTCTGAACACGCTGCAGTTCAACATGTCTGTTCCAACACCTTATGTCTTCATGAAGAG 1004
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                                                                                                     493 GATTCTGAACACGCTGCAGTTCAACATGTCTGTTCCAACCCCTTATGTCTTCATGAAGAG 434
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855 California Ave, Palo Alto, CA 94304, USA
1781: 650 723 2227
Fax: 650 725 8221
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Plate: 687075 row: H column: 12.
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Department of Biological Sciences
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/clone_lib="687 - Early embryo from Delaware"
/note="Organ: embryo; Vector: pBluescript SK; Site_1:
Xho!; Site_2: EcoRi; Library was prepared by Statagene
using the Uni-2AP RK system (Stratagene BN937328-12).
Clones were picked by a Q-bot after blue/white selection
(ampicullin resistance - use 100 micrograms/microliter).
Developed from a pool of equal amounts of RNA from
developing embryos sampled at 14, 21, 28 and 35 days after
pollination of the Illinois High Oil Maize Strain Cycle
90. This closed strain has been selected for high oil
concentration for 90 generations and originates from the
1890s era open pollinated variety Burr's White"
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CD001830 579 bp mRNA linear EST 01-MAY-2003 3529 1 104 1 D01.y 13529 - 2 mm ear tissue from Schmidt and Hake labs Zea mays CDNA, mRNA sequence.
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1 (bases 1 to 579)
Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4577"
/tissue_type="ear"
/dev_stage="2 mm"
/lab_host="2 coli XLOLR"
/clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: ear, Vector: PAD-GAL4-2.1; Site 1: EcoRI
Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu
amplified. Ampicillin is the selection marker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCCCATGACAAGGAAATTCGCCGCCTCCTTGGCGAGCAAGGGCCAACCTGAATGTCAG
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Contact: Walbot V.

Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, US/
Tel: 650 723 227

Fax: 650 725 8221

Email: Walbot@stanford.edu

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/mol type="mRNA"
/cultivar="B73"
                                                                                                                        CD001830.1 GI:30307157
                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                               Zea mays
Zea mays
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Best Local S:
Matches 579,
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Contact: Walbor (1999)
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Stanford University Palo Alto, CA 94304, USA 855 California Ave, Palo Alto, CA 94304, USA Tal: 650 725 8221
Eax: 650 725 8221
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                                                           1. .663
/organism="Saccharum officinarum"
Seg primer: T7 Promoter Primer
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al Similarity 92.5%;
613; Conservative
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AI770352 S86 bp mRNA linear EST 02-FEB-2000 605661D02.x1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence. ö 672 180 240 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Pepermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea. agagaaaarcaggcraagagrrgrgraaacccrgarracargrccagrcagcaagarara 120 732 GTGGTTCCAAGGAAGAAGCTACAACTGGTTGGAGTCACAGCTATGCTGCTCGCTTGTAAA 852 241 Gridericcia i de de la comita del comita de la comita del comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita de la comita del comita de la comita de la comita della comita 912 301 Tangaggaggreneaghrecaghtarngaggacerngrecreannergacegreechae 360 ACAAAAGGGCAAATTTTAGAAATGGAAAAGTTGATTCTGAACACGCTGCAGTTCAACATG 972 9 /note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt lab" /organism="Zea maye" /mol type="mRNA" /cultivar="Ohio43" /db_xref="taxon:taxon:tase" /tissue type="mixed" /dev_stage="ear length from 0.5 cm - 2.0 cm" /lab_host="XIOLR (Strategene)" /clone_lib="606 - Bar tissue cDNA library from Schmidt lab" GCAGACTCGGGGAACCCGCTTGCAGCAACAGAATATGTTGAAGAGGCTTTACAAGTTTTAC AATGCAAAGATGAGGAATTCTGATTGACTGGCTGATTGAGGTTCACTACAAGTTTGAA 553 GCAGACTCGGGGAACCCGCTTGCTGCAACAGAATATGTTAAAGAGCTTTACACCTTTTAC 613 AGAGAAAATGAGGCTAAGAGTTGTGAAGGCCAGATTACATGTCCAGCCAACAAGACATA **AACTCAAAGATGAGAGCAATTCTGATTGACTGGCTGATTGAGGTTCACTACAAGTTTGAA** TATGAGGAGGTATCTGTTCCAGTTGTTGAGGACCTTGTGCTGATATCTGACCGTGCCTAC Gaps Walloct, V. Maize ESTs from various cDNA libraries sequenced at Stanford ; 0 Score 531.6; DB 9; Length 586; Pred. No. 4e-70; 0; Mismatches 34; Indels 0

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CCTTATGTCTTCATGAAGAGGTTTCTGAAAGCTGCAGATGCAGATAAAACAGCTTGAGCTA 1044
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CA122563.1 GI:34975871
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                                        TCTGTTCCAACACCTTATGTCTTCATGAAGAGGTTTCTGAAAGCTGCAGATGCAGATAAA 1032
                                                                                          CAGCTIGAGCTAGCGICATTITICATGCTGGAGCTCTGCTTGGTAGAATACCAAATGCTG 1092
                                                                                                                                                                                                                                                                                                                 Saccharum officinarum
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Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Sukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; FACCAD
Salda; Panicoideae; Andropogoneae; Saccharum.
(bases 1 to 742)
Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P.
Halbrariee that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
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ACAAAAGGGCAAATTCTAGAAATGGAAAAGTTGATGATCTGAACACGCTGCAATTCAACATG
                                                                Query Match 31.3%; Score 512.6; DB 13; Length 742; Best Local Similarity 89.4%; Pred. No. 2.5e-67; Matches 613; Conservative 0; Mismatches 55; Indels 18; Gaps
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Universidade Estadual de Campinas
Universidade Estadual de Campinas
Caixa Postal 6100, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: partuda@unicamp.br
Clone distribution: clone distribution information can be funcugh the Brazilian Clone distribution Conter (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 033 row: H column: 06
Seq primer: SPG Promoter primer.
                                                                                                                                              1093 AATTATCGGCCTTCGCATCTGCTGCTGCGGTTTATACTGCAC 1138
                                                                                                                                                           541 AATTATAGGCCTTCACATCTGGCTGCGCTGCGGTTTATACTGCAC 586
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Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicocideae; Andropogoneae; Saccharum.
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Contact: Arruda P
Contact Batadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1189
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
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SCJFFL1C03E09.b FL1 Saccharum officinarum cDNA clone SCJFFL1C03E09
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682 cerrangraricardaadagrarinerdaaaderdeeadardedagaraceaderroadeaa
                                                         GCGTCA-TTTTTCATGCTGGAGCTCTGGTTAGAATA-CCAAATGCTGAATTATCGGC
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CA223571
CA223571.1 GI:35280031
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OGVGS27TV ZM 0.7_1.5 KB Zea mays genomic clone ZMMBMa0478F05,
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                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

(Dases 1 to 778)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Other GSSs: OGYOSZ7TH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207
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Strain="873"
/db_xxef="taxon:4577"
/clone="ZNMBMa0478F05"
/clone="ZNMCFOF"
/note="Wocror: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation_filtered_genomic_DNA_library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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9712 Medical Center Drive, Rockville, MD 20850,
                                                                                                                                              Zea mays
Zea mays
Eukaryota, Viridiplantae, Streptophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                      CG453107.1 GI:34838107
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/lab_hose="DHIOR"
/lone lib="Ftl"
/note="Crgan: Inflorescence at begining of development
/note="Crgan: Inflorescence at begining of development
/lone-long); Vector: pSport1; Site_1: Sal1; Site_2: NotI;
An unidirectional cDNA library generated from
[Inflorescence at begining of development (lon-long)]
CDNA was prepared from polyA+ mRNA using SuperScript
Plasmid System Kit (Invitrogen). The double-strand cDNNs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 Kb were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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                                                                                    organism="Saccharum officinarum"
Plate: C03 row: E column: 09
Seg primer: SP6 Promoter primer.
Location/Qualifiers
                                                                                                    /mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJFFL1C03E09"
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CG278953 873 bp DNA linear GSS 25-AUG-2003 OGZAT49TV ZM 0.7_1.5 KB Zea mays genomic clone ZMMBMa0659J02, genomic survey sequence.
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1 (bases 1 to 873)
Whitelaw, C.A., Puscer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSSs: OGZAT49TH
631 CGTTGCCAGCACTGGACAAAGGTCTGCGAGTCTCATAGCAGATACACTAGCGACCAACTC 572
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                                                                                                                                               511 CIGIGIGIACCTITIGCIGIICICACCAGGAGIGCICGAGGAIGAIGAIGGIAGAITITCAC
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                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD 20850, USA
Fer: 301-838-8543
Fax: 301-838-0208
Email: whitelaw@tigr.org
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/strain="B73"
/db_xref="taxon:4577"
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1 (Dasea 1 to 779)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Other GSSs: OGVGS27TV
Contact: Cathy Whitelaw
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                                                                                                                                          CGGTCGGTCACGTTGTGCTTGTGCAGTTATACTGCGGCTAATAACAAAACTGTCCAGTTAT
  CCTTCAGGTGCAAACTAGTTGAATCGACCTATTCAACTGGGTGGATTTTTAAAGTTTTT
                                        AGAATACTCCATGAACAAGATGCAGAAAACATCGTGTTGATGTTGCCCAAAAGTGCATCG
                                                                          508 AGAATACTCCATGAACAAGATGCAGAAACATCGTGTTGATGTTGCCCAAAAGTGCATCG
                                                                                                                     Gaps
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/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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/strain="B73"
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/clone="ZMMBMa0478F05"
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Class: sheared ends.
Location/Qualifiers
1. 775
/organism="Zea mays".
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Saccharum officinarum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum.
                                                                                                        Gaps,
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                             3
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation_filtered_genomic_DNA_library"
                                                                                                        87;
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5', mRNA sequence.
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/clone_lib="HRI"
/note="Grapan: seedlings inoculated with Herbaspirilum
rubrisubalbicans; Vector: pSport1; Site_1: Sal1; Site_2:
Not1; An unidirectional cDNA library generated from
[seedlings inoculated with Herbaspirilum
rubrisubalbicans]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be f
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 015 row: C column: 10
Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.5%; Score 482; DB 13; Length 626; llarity 88.5%; Pred. No. 1.1e-62; Conservative 0; Mismatches 45; Indels 27
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/lab_host="DH10B"
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Search completed: March 20, 2004, 23:04:32 Job time : 4453 secs